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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
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Perfect score:
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                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
                                                                                                                                                                                                                                                                                                                                                                                                                         seq
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Query
Match
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Gapop 10.0 , Gapext 0.5
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294
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sp_organelle:*
sp_phage:*
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sp_fungi:*
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                                                                                                                                                                                                                                                   sp_mammal:*
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sp_virus:*
sp_vertebrate:*
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   띪
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 IJ
                                            SUMMARIES
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Description
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25.5	25.9	25.9	25.9	)	27.7	29.4	31.5	31.5	31.6	34.7	34.9	36.4	37.8	39.5	39.6	41.7	42.0	42.5	42.5	55.4	57.5	58.8	60.2
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009123 Q9DVT5	022837	Q9BVZ4	009120	009119	8MSQ60	Q9GLN5	Q9PYQ9	Q9DDK0	61WA60	Q9YKL5	Q9PZ54	055770	092394	Q9YVJ4	088738	Q9VEM2	Q9VH01	Q91F18	Q9E232	Q9VUX5	Q9QES9	Q9J827	Q9EQ04
009123 mus musculu 09dvt5 plutella xy	_	Q9bvz4 homo sapien	009120 mus musculu	11	Q9dsw8 ascovirus d	Q9gln5 sus scrofa	Q9pyq9 xestia c-ni			Q9ykl5 epiphyas po		055770 chilo iride	092394 bombyx mori	Q9yvj4 melanoplus	O88738 mus musculu	Q9vem2 drosophila	Q9vh01 drosophila	Q9ifi8 helicoverpa	Q9e232 helicoverpa	Q9vux5 drosophila	Q9qes9 epiphyas po	Q9j827 spodoptera	Q9eq04 rattus norv

## ALIGNMENTS

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RESULT
Q9UNH1
     Interpro; IPR001370; BIR.
Interpro; IPR001370; Gaspase.
Interpro; IPR001398; Ig_22.
Interpro; IPR001358; Ig_22.
Interpro; IPR003508; Ig_Hke.
Interpro; IPR003508; Ig_Hke.
Interpro; IPR003508; Ig_HKC.
Pfam; PF00633; BIR; 3.
Pfam; PF00047; Ig; 2.
SMART; SM00238; BIR; 3.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00410; IG_Like; 1.
PROSITE; PS01428; BIR_REPEAT_1; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9UNH1 PRELIMINARY;
O9UNH1;
O1-MAY-2000 (TrEMBLrel. 1:
O1-MAY-2000 (TrEMBLrel. 1:
O1-JUN-2001 (TrEMBLrel. 1:
API2-MLT FUSION PROTEIN.
                                                                                                                                                                                                                                                                          Dierlamm J., Baens M., Wlodarska I., Stefanova-Ouzounova M., Hernandez J.M., Hossfeld D.K., De Wolf-Peeters C., Hagemeijer A., Van den Berghe H., Marynen P., The apoptosis Inhibitor gene API2 and a novel 18q gene, MLT, are recurrently rearranged in the t(11:18)(q21;q21)p6ssociated with mucosa-associated lymphoid tissue lymphomas.";
Blood 93:3601-5609(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human),
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhiní; Hominidae; Homo.
                                                                                                                                                                                                                                  EMBL; AF123094; AA
HSSP; Q13490; 1QBH
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-99272400; PubMed-10339464;
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                                                                                                                                                                                                                                                                  DOMAIN
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Last sequence update)
Last annotation update)
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1140 195 602 589 589 224 224 228 237 276 377 597

Q9EN27

Ogunhi homo sapien
Qojiafo gallus gall
Ogiafo gallus gall
Ogiafo gallus gall
Ogosep rattus norv
Ogosef rattus norv
Ogosef rattus norv

Q9UNH1
Q9IA70
Q9IA69
Q9E7319
Q9ESEB
Q9ESEB
Q9DDN2
Q8E642

Q9HAP7 2 Q9YNL8 2 Q9H2A8 Q9H2A4

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Q90492 Q9NJ07 Q9R015 Q9ESF0 Q9EQ05

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RESULT 3

Q91A69
Q91A69
AC Q91A69
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-UN-2001 (TrEMBLrel. 17, Last annotation update)
DT 01-UN-2001 (TrEMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS 1 (FRAGMENT).
OS Gallus gallus (Chlcken).
OC Eukoryota: Metazoa: Chordata: Craniata: Vertebrata: Euroccentric States (Chicken).
OC Archosauria: Aves: Neognathae: Galliformes: Phasianidae
OC Gallus.
ON NCBLTaxID-9031;
RP SEQUENCE FROM N.A.
RC STRAIN-BREED FAYOUMI: TISSUE-SPLEEN:
RA Zhou H., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian st specific ganes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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O91A70:
O91A70:
O91A70:
O91CT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF ADOPTOSIS 1 (FRAGMENT).
Gallus gallus (Chicken).
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Best Local
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NON_TER
SEQUENCE
                              "Genetic variation among chicken lines and mammalian species specific genes.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00238; BIR; 2.
pROSITE; PS01282; BIR_REPEAT_1;
pROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specific genes.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF221082: AAF35319.1;
InterPro; IPR001370; BIR.
Pfam; PF00653; BIR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BREED LEGHORN; TISSUE-SPLEEN; Zhou H., Lamont S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genetic variation among chicken lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PEQLASAGFYYYGNSDDVKCFCCDGGLRCWESGDDDWVQHAKWFPRCE 48
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           sted (JAN-2000) to the EMBL/GenBank/DDBJ databases {\tt AF221083}; {\tt AAF35320.1}; -.
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22347 MW;
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Pred. No. 9e-29;
3; Mismatches
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Pred. No. 3.3e-30;
; Mismatches 0;
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nes; Phasianidae; Phasianinae;
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           RESULT OF THE PROPERTY OF THE 
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Best Local S
Matches 43
                                                                         Pfam; PF00053; BIR; 3.

Pfam; PF00059; CARD; 1.

Pfam; PF00097; Zf-C3HC4; 1.

SMART; SM00238; BIR; 3.

SMART; SM00114; CARD; 1.

SMART; SM00184; RING; 1.

SMART; SM00184; RING; 1.

SMART; SM0184; RIR; REPEAT_1; 3

PROSITE; PS01282; BIR_REPEAT_1; 3

PROSITE; PS50143; BIR_REPEAT_2; 3

PROSITE; PS50209; CARD; 1.
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Pfam; Pf00653; BIR; 2.

SMART; SM00238; BIR; 2.

SMO23TE; PS01282; BIR_REPEAT_1; 2

PROSITE; PS50143; BIR_REPEAT_2; 2

NOM_TER 1 1 17

NOM_TER 197 AA; 22602 MW; D7
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057319;
01-JUN-1998 (TrembLrel. 06, Created)
01-JUN-1998 (TrembLrel. 06, Last sequence update)
01-JUN-2001 (TrembLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF T CELL APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                        -!- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC
-!- SIMILARITY: MEMBER OF THE IAP FAMILY.
-!- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION APOPTOSIS PROTEIN REPEAT)
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; AF008592: AABB8044.1; -.
HSSP: Q13490; 10BH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98038801; PubMed-9372964; You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.; You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.; Ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is medlator of the antiapoptotic activity of the v-Rel oncoprotein."; Mol. Cell. Biol. 17:7328-7341(1997).

-I- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
           Apoptosis;
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-WHITE LEGHORN; TISSUE-EMBRYONIC FIBROBLAST:
                                                                                                                                                                                                                                                                                                               InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF THE V-REL-TRANSFORMED CELLS.
THE V-REL-TRANSFORMED CELLS.
TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE SPLEEN, THYMUS, BURSA, IMPESTINE, AND LUNG, AND AT VERY LOW LEVELS IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
           Zinc-finger; Repeat.
30 97 81
176 242 BJ
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Pred. No. 9.1e
3; Mismatches
              BIR
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V-REL-TRANSFORMED

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Best Local S
Matches 43
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Best Local
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                                                                                              O9DZC6 PRELIMINARY; PRT; 589 AA.
O9DZC6;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence upda
O1-JUN-2001 (TrEMBLrel. 17, Last annotation up
INHIBITOR OF APOPTOSIS PROTEIN 2.
RATTUS norvegicus (Rat).
RATTUS norvegicus (Rat).
EUKARYOTE, Metazoa: Chordata; Craniata; Verreb
BUKARYOTE, BUTHERIA; RODENTIA; Sciurognath; Mu
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00114; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 1
PROSITE; PS05143; BIR_REPEAT_2; 3
PROSITE; PS50209; CARD; 1.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
17HIBITOR OF APOPTOSIS PROTEIN 1.
Rattus norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

"Cloning and Characterization of the Rat Homologs of the
Apoptosis Protein 1, 2, and 3 Genes.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

EMBL; AF18340; AG222970.1;

InterPro; IPR001370; BIR.

InterPro; IPR001315; CARD.

InterPro; IPR001315; CARD.

InterPro; IPR001841; Znf_ring.
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SEQUENCE
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   SEQUENCE FROM N.A.
                                                                NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00653; BIR; 3
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nes 43; Conser
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43; Conser
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563
610
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Pred. No. 2.9e-28;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 276; DB Pred. No. 3.9e 4; Mismatches
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C3HC4-TYPE.
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                                                                                                                                        Vertebrata;
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.9e-28;
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RESULT
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A HOLCIK M., Lefebvre C.A., Hicks K., Korneluk R.G.;

A HOLCIK M., Lefebvre C.A., Hicks K., Korneluk R.G.;

Tholois M., Lefebvre C.A., Hicks K., Korneluk R.G.;

Tholois Protein 1, 2, and 3 Genes.";

Lefebvre C. and 3 Genes.";

Lefe
                                                             Query Match
Best Local Similarity
Matches 42; Conserv
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Best Local
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Pfam; PF00697; CARD; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
PROSITE: PS01282; BIR_REPEAT_1; 3
PROSITE: PS01282; BIR_REPEAT_2; 3
PROSITE: PS0143; BIR_REPEAT_2; 3
PROSITE: PS0143; BIR_REPEAT_2; 3
PROSITE: PS0143; BIR_REPEAT_2; 3
PROSITE: PS0209; CARD; 1.
Zinc-finger.
SEQUENCE 589 AA; 66777 MW; E6
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Q9ESE8;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence up
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation
UNHIBITOR OF APOPTOSIS PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                         PROSITE; PS01282; BIR_REPEAT_1; PROSITE; PS50143; BIR_REPEAT_2; PROSITE; PS50209; CARD; 1.
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InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=KIDNEY;
Dong Z., Dento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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nilarity 87.5%;
Conservative
                                                                                                                                                                                                                               589 AA;
                                                                                                                                                                                                                                   66750 MW;
                                                                                             91.8%;
87.5%;
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                                                                 Score 270; DB
Pred. No. 2.4e
4; Mismatches
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Pred. No. 2.4e
4; Mismatches
                                                                                                                                                                                                                                   B4F7089BD7CD285B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E6812FFE3EA34142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ωω
                                                                 DB 11;
2.4e-27;
nes 2;
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.4e-27;
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                                                                                                                                     589;
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                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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PEQLASAGEYYVDHNDDVKCFCCDGGLRCWEPGDDPWIEHAKWFPRCE 306

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Best Local S
Matches 40
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P T'The apportosis inhibitor ch-IAPl is a direct transcription:

T v-Rel and c-Rel.";

V-Rel and c-Rel.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

B SUBMITTER 1311289; AG642316.1; -.

R InterPro; IPR001370; BIR.

P FAME; PF301289; BIR; 3.

PROSITE: PS001281; BIR; 3.

PROSITE: PS01282; BIR_REPEAT_1; 1.

PROSITE: PS01282; BIR_REPEAT_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DDN2 PRELIMINARY; PRODUNT; PRELIMINARY; PRODUNT; PRELIMINARY; PRODUNT; PREMBLEE! 16, Careated) 01-MAR-2001 (TrEMBLEE! 16, Last sequence update) 01-JUN-2001 (TrEMBLEE! 17, Last annotation update) APOPTOSIS INHIBITOR CH.1AP1 (FRACMENT).
Gallus gallus (Chicken), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-OVARY, CORPUS LUTEUM;
Bradley C.K., Lareu R.R., Dharmarajan A.M.;
"Cloning and characterisation of an inhibitor of apoptosis
"Cloning and characterisation of an inhibitor of apoptosis
"(IAP) in the rat corpus luteum.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFOB1503; AAC32497.1; -.
EMBL; AFOB1503; 10BH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota: Metazoa: Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O88642 PRELIMINARY; PRT; 224 AA.
088642;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                           Pfam; PF00653; BIR; 2.
SMART; SM00238; BIR; 2.
PROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIAP1.
                                                                                                                                                                          InterPro; IPR001370; BIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 PEQLADAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWIEHAKWFP
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      224
224
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      3
      224
25209
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      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5E2B89DEAE3733F3
      213A52534D5EB56A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258; DB 13;
No. 4.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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Best Local S
Matches 31
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF250284; AAG02727.1; -.
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 2.
SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; PS50143; BIR.REPEAT_2; 2
SEQUENCE 264 AA; 30547 MW; 2E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9EN27;
Q9EN27;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                      Q9HAP7 PRELIMINARY; PRT; 280 AA.
Q9HAP7;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
LIVIN INHIBITOR-OF-APOTOSIS (INHIBITOR OF APOPTOSIS) (BA261N11.1.1)
(BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 7 (LIVIN), ISOFORM 1).
LIVIN OR BIRCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20396580; Pubmed-10936094;
MEDLINE-20396580; Pubmed-10936094;
TAY OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus: Analysis and Comparison with Other Poxviruses."; Virology 274:120-139(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=28321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amsacta moorei entomopoxvirus (AmEPV). Viruses; dsDNA viruses, no RNA stage; Entomopoxvirus B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moyer R.W.;
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bawden A.L., Glassberg
Moyer R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMV021
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                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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31; Conser
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33; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (TrEMBLrel.
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l (TrEMBLrel.
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66.0%;
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16,
17,
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Pred. No. 9e-19;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Pred.
                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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2EB72DA4B58D920A CRC64;
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No. 3.1e-19;
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                                                  family member.";
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Best Local S
Matches 32
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A L SUBmitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
R EMBL; AF311388; AAG33622.1; -.
R EMBL; AL121827; CAG36112.1; -.
R InterPro; IPR001370; BIR.
R InterPro; IPR001841; Znf_ring.
R InterPro; IPR001841; Znf_ring.
R Ffam; PF00057; Zf-C3HC4; 1.
R Pfam; PF00057; Zf-C3HC4; 1.
R SMARR; SM00184; RING; 1.
R SMARR; SM00184; RING; 1.
R PROSITE; PS50143; BIR, REPEAT_2; 1.
R PROSITE; PS50143; BIR, REPEAT_2; 1.
R PROSITE; PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1.
O SEQUENCE 280 AA; 30866 MM; 630BE9C0737F7952 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.0
Best Local Similarity 60.0
Matches 29; Conservative
                                                                                                                                                                                                         "CFMNPY IAP gene.";
SUBMITTED (DEC-1996) to the EMBL/G
-!- SIMILARITY: CONTAINS A RING-TY
EMBL; U82510; AAD00537.1; -.
HSSP; Q13490; 1Q8H.
InterPro; IPR001841; Znf_ring.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 2.
Pfam; PF00057; Zf-C3HC4; 1.
SMART; SM00238; BIR; 2.
SMART; SM00244; RING; 1.
PROSITE; PS0143; BIR_REPEAT_1; UN
PROSITE; PS0143; BIR_REPEAT_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9YNL8;
Q9YNL8;
01-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashhab Y., Alian A., Polliack A., Panet A., Ben-Yehuda D.;
"Two splicing variants of a new inhibitor of apoptosis gene with
different biological properties and tissue distribution pattern.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choristoneura fumiferana nuclear polyhedrosis virus (CfMNPV) Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CfMNPV TAP gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Conservative
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                                      65.6%;
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Score 193; DB Pred. No. 1.5e 3; Mismatches
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Last sequence update)
Last annotation update)
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RING-TYPE ZINC FIN
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Pred. No. 1.5e
9; Mismatches
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                                                                                                                                                                                 B2D9BE8A359F105E
                                                                                                                                                                                                                                                       UNKNOWN_1
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.5e-17;
                              DB 12;
.5e-17;
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                                                                                                                                                                                 CRC64;
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                                                                     Length 281;
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       9
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29 H2MI 20 H2M
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

C -- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

R EMBL; AB301009; AAG37878.1; --

R EMBL; AJ309298; CAC37338.1; --

R EMBL; AJ309298; CAC37338.11.1; --

R InterPro; IPR001370; BIR.

R InterPro; IPR001370; BIR.

R Pfam; PF00653; BIR; 1.

R Pfam; PF00653; BIR; 1.

R Pfam; PF00097; zf-C3HC4; 1.

R SMART; SM00184; RING: 1.

R SMART; SM00184; RING: 1.

R PROSITE; PS00184; RING: 1.

R PROSITE; PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1.

V Zinc-finger.

SEQUENCE 298 AA; 32798 MW; B2EAAEE531BEC101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 29; Conser
                                                                                                                                    089744 PRELIMINARY;
089744;
01-NOV-1998 (Tremblrel 08, 0
01-NOV-1998 (Tremblrel 08, 1
01-JUN-2001 (Tremblrel 17, 1
APOPTOSIS INHIBITOR IAP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Ashhab Y., Alian A., Polliack A., Panet A., Ben-Yehuda D.;
Ashhab Y., Alian A., Polliack A., Panet A., Ben-Yehuda D.;
"Two splicing variants of a new inhibitor of apoptosis gene with
different biological properties and tissue distribution pattern."
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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O9H2A8;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN KIAP (BAZGINII.1.2)
REPEAT-CONTAINING PROTEIN 7 (LIVIN), ISOFORM 2).
Buzura suppressaria nuclear polyhedrosis virus (BsNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID-74320;
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Lin J.-H., Deng G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem.
                                                                                                                  IAP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                   PELLAAAGFFHTGHQDKVRCFFCYGGLQSWKRGDDPWTEHAKWFPSCQ 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Deng G., Huang Q., Morser J.; member of the inhibitor of apoptosis Biophys. Res. Commun. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.68;
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9; Mismatches
                                                                                                                                                               Created)
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Last anno
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                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                  sequence update) annotation update)
                                                                                                                                                                                                                                                                              276
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..6e-17;
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RESULT
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                                                                                                                                                                                                                                                                                                                           RP SEQUENCE FROM N.A.

XA MEDITINE-20062908; pubMed-10593985;

AA Seshagiri S. Vucic D., Lee J., Dixit V.M.;

AB Seshagiri S., Vucic D., Lee J., Dixit V.M.;

AT 100 Minimum M
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Best Local Similarity 63.8
Matches 30: Conservative
                                                                                                                                       Query Match 65.0%;
Best Local Similarity 63.8%;
Matches 30; Conservative
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Interpro: IPRO01370; BIR.
Interpro: IPRO01841; Znf_ring.
Pfam; PF00053; BIR; 2.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00128; BIR; 2.
SMART; SM00184; RING; 1.
PROSITE; PS01288; BIR_REPEAT_1; UPROSITE; PS01288; BIR_REPEAT_2; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9U492 PRELIMINARY; PRT; 379 AA. Q9U492; O1-MAY-2000 (TrEMBLrel. 13, Created) O1-MAY-2000 (TrEMBLrel. 13, Last sequence update) O1-JUN-2001 (TrEMBLrel. 17, Last annotation update) INHIBITOR OF APOPTOSIS PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98376358; PubMed-9712513;
Hu Z.H., Arif B.M., Sun J.S., Chen X.W., Zuidema D., Goldbach R.W.,
Vlak J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trichoplusia ni (Cabbage looper).
Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota: Neoptera: Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea: Noctuidae: Plusiinae: Trichoplusia.
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SEQUENCE 276 AA;
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-7111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
227
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PEELAEAGFFYTGQGDKTKCFYCDGGLKDWENDDVPWEQHARWFDRC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%;
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Pred. No. 2.6e-17;
5; Mismatches 12; Indels
                                                                                                                                       Score 191; DB 5; Length 379; Pred. No. 3.7e-17; 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C467275E58D36422 CRC64;
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